

SEQUENCE LISTING

<110> Habben, Jeffrey E.
Zinselmeier, Christopher
Tomes, Dwight
Abbitt, Shane
Helentjaris, Timothy G.
Niu, Xiaomu

<120> Modulation of Cytokinin Activity in
Plants

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<150> US 60/460,718
<151> 2003-04-04

<150> US 09/545,334
<151> 2000-04-07

<150> US 60/129,844
<151> 1999-04-16

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1

5

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Leu Ser Thr Gly Ser Gly Arg Pro Thr Val Glu Glu Leu Lys Gly Thr			
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Gln Ile Thr Pro Asp Met Leu Leu Gln Leu Asp Ala Asp Met Glu Asn			
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235			

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<213> *Agrobacterium tumefaciens*

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65          70          75          80
Ile Ala Glu Val His Asn His Glu Ala Lys Gly Gly Leu Ile Leu Glu
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Gly Gly Ser Ile Ser Leu Leu Arg Cys Met Ala Gln Ser Arg Tyr Trp
          100          105          110
Asn Ala Asp Phe Arg Trp His Ile Ile Arg Asn Glu Leu Ala Asp Glu
          115          120          125
Glu Ser Phe Met Ser Val Ala Lys Thr Arg Val Lys Gln Met Leu Arg
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Pro Ser Ala Gly Leu Ser Ile Ile Gln Glu Leu Val Gln Leu Trp Arg
145          150          155          160
Glu Pro Arg Leu Arg Pro Ile Leu Glu Gly Ile Asp Gly Tyr Arg Tyr
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Gln Leu Asp Ala Asp Met Glu Asn Lys Leu Ile His Gly Ile Ala Gln
          195          200          205
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<212> DNA

<213> *Zea mays*

<220>

<221> promoter

<222> (1) ... (2085)

<223> zag2.1

<400> 3

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<213> Cauliflower mosaic virus

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<221> enhancer

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<223> CaMV35s

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<210> 5

<211> 2198

<212> DNA

<213> Zea mays

<220>

<221> promoter

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<223> ZmMADS

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<213> Zea mays

<220>

<221> promoter

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 <213> Zea mays

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 aagttagcta gctctggtcg cgctaacttc tgtcgatcgc ctattagcta atactccatc 660
 tgtcccatta tataaggtat aaccaactct gattcaaaga ccaaaaatat acttaattgt 720
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 aagaacaaaa atattggttac gccttatatt ataagacgta gaaatcaatg gtttacaata 840
 gccagaata gatgttttta tttatttctt atatagatgt ttttatttat ttctatatg 900
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 tgtactccgc gcgtattacc atgcactacg acgtacgtag gagtatgtac gttgaaccaa 1020
 gcacacatat atctctgaca cagtacaatg atatactaca acaacaacag tactgcccac 1080

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cgacgacgga	gcagtacttc	acagaatcct	ccgccactcg	tcacaccaac	aggcgcgcg	1200
tggtgcat	gcacatgtg	catgccatcg	tccgtccctt	ggcgtgcctc	ggtagacggt	1260
agctagagta	gtagcctgtg	cttgctaccc	ctgggtcaaca	catcgtagcc	tcctatatatt	1320
aacgtatcct	cacacatcac	aagaacgaca	cacagaaacc	agtagccact	actccatcca	1380
ccacgagcga	gcgagcgata	accctagcta	gcttcaggat	ccagcgagag	ccc	1433

<210> 10
 <211> 820
 <212> DNA
 <213> Zea mays

<220>
 <221> promoter
 <222> (1) ... (820)
 <223> F3.7 promoter

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gaagtggaga	agaggtccgg ctggtggcat cctatcgtct attgaggggt gggtcgggtg 180
gcatacact	tgatgacaat tgaaagtaat tttaataaac ttgtcatgag tagtgagtct 240
tttataaaaa	ataagctgaa ataagcacc tttgatgagc ttataggatt atcataatct 300
caaagtctaa	attatataat ttatttagat aagttgcttg tttgtttccc cactagctta 360
tttacattgg	attatataat ctacataaat tataatctca aacaaaaagt ccttaatcag 420
agatcagcga	ggtctcacga gtgagaaggc gagagcttgt ccaaacgagc attttcgggc 480
gtgtgaacac	ccatttcagc aaagccgctg ttgtccagtt cagcgaagcg cattctgcgg 540
ctttggcggtg	accatttctg ctagctcagc actgagaata cgcgtccgct gcagcgttgg 600
cgtacaggcc	ggactacatt agccaacgcg tatcggcagt ggcaaacctc ttcgcttcta 660
actccgctgg	gccaccagct ttgaccgccc cctcccttcc cctccgctac tgctcctccc 720
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<210> 11
 <211> 26
 <212> DNA
 <213> Zea mays

<400> 11		
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<210> 12
 <211> 26
 <212> DNA
 <213> Zea mays

<400> 12		
tcgcccagaa	gaagcagcag	gaagat 26

<210> 13
 <211> 26
 <212> DNA
 <213> Zea mays

<400> 13		
aagcttaggg	tacctcaaac	cggtca 26

<210> 14

<211> 34
 <212> DNA
 <213> Zea mays

 <400> 14
 ccatgggtcga tatcttttgca gggtagggat ctct 34

 <210> 15
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Clontech AP1 primer

 <400> 15
 gtaatacgac tcactatagg gc 22

 <210> 16
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Clontech AP2 primer

 <400> 16
 actatagggc acgcgtggt 19

 <210> 17
 <211> 1679
 <212> DNA
 <213> Zea mays

 <220>
 <221> promoter
 <222> (1) ... (1679)
 <223> tb1 promoter

 <400> 17
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 aggaaaggga agttagttgg tcattatctt tgttgatgcc tcaacatgta attttcttcg 180
 ccattgtatt tctcaatcca ctatatacaa agagggtata gggatatatat tacacatctt 240
 acggtccgaa cctatattta aattacccat gtattgatgc ctaggcggta tccagcaaca 300
 gagtgtctct agcacgcatc tcttactcta tttatcaact ctccccgaa tacatgtggt 360
 tccttattgt cactggcgga tctacagggt gtcaccctgt agtccgggtac cggcataaca 420
 tattagcttt gtctatttca tgacttcaaa catggttgcaa caacctacag atgcgttcag 480
 tctatctata tacaagagga agaatacaag tgacaaatct aatttgtgaa tataagaatt 540
 attatgctgg ttacataga ataccaaatt atagcacaca tttatcattc cttattgaat 600
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 tggaggcgcg cacgtccatc gtactgcgtc ctgcagctat ggccgcccc atctggccaa 1080

taaagtact	aggtcacttg	tagccaatag	cgtttcaaca	tgcacacagc	ttttcccca	1140
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atcaacacac	actgctctta	gtgccaggac	ctagagaggg	gagcgtggag	agggcatcag	1620
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<210> 18

<211> 1027

<212> DNA

<213> Zea mays

<220>

<221> promoter

<222> (1)...(1027)

<223> eep2 promoter

<400> 18

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ctcggttcaa	aattttattag	attatataat	ccatacatat	tacaatccca	aacaaacacc	180
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tatgtcccag	taactaaata	ctatatattgt	caccataaac	tttgggaagaa	attagttgct	420
actagaaaga	agatccaaac	ctggaaaaaa	ttagttttcta	ctagaaagca	gatcatgtct	480
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ttggaagaaa	ttagttgcta	ctagaaagta	gataattttct	gccaccagat	attgattttat	600
aacctagtat	caatctctac	tagccttgct	tcggtcattt	gttgctagat	ataaatgggt	660
ttctttcaca	tatgtgagtg	tatatatatg	aaccttgcag	caaccattat	attcggtagt	720
caaacaagc	cctacagaca	tcgatctctg	atctgagaaa	aaaaatcctt	atatggcgag	780
aattacaatg	gaagcaagca	aggctgtcct	gctcttgatg	gtgatcctag	gaagtttgat	840
gattcccgca	tactgtgaagt	gcacatcggg	caaccatgcg	catttgaatc	aagttacata	900
ttatacagtt	tcttactagt	agtaaatata	aattgttcgc	ataatgtcaa	caaccttaac	960
ttactgtaaa	aacagtaact	gaatgccctt	attgcatgca	gctcggaacc	ttgttcgttt	1020
tctgccc						1027

<210> 19

<211> 723

<212> DNA

<213> Zea mays

<220>

<221> promoter

<222> (1)...(723)

<223> trxl or thxH promoter (thioredoxin H)

<400> 19

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gatgcactgg	cgttcatttg	cggctgtggt	aacaaaaccg	aagtggaggt	agcccggtcc	180
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acacaactgt	cagtataaat	agtttttttt	attggcggtt	gatttaggtg	aaccccaagc	300
gaaaatatat	ttacacatgc	ggttttttta	gccgtgctca	cctattttatt	ttcagtgtgc	360

ttaactgaaa	ctgtcgggat	aaatTTTTGc	gtgccatcag	tttagagcac	ttatctactg	420
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cacgccgatc	tagagagctc	gaagacctgg	gaatggcaca	ggggaccggc	cggagcccg	540
cggcgccatg	caagctgcct	cgatcgcggg	cctcgacctc	agtagcccg	ccctgtcgcg	600
cgccagtcgc	tcgctgcgcc	tataaaagcc	gcccgcggct	cgcgtaggct	accagcgcaa	660
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atg						723

<210> 20
 <211> 1626
 <212> DNA
 <213> Zea mays

<220>
 <221> promoter
 <222> (1) ... (1626)
 <223> Zm40 or Mze40-2 promoter

<400> 20						
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ccgtgtcatg	gttttgtaga	cacgtttacg	tatcaattat	agtgttctga	ttttttatat	240
tctcctaatt	atttagagct	aaatTTtatt	ttatgatagc	agagatctaa	atatttttgt	300
tttgattttt	tatatactaa	aatcatctct	acaatattag	agatttttaa	tgctcagaag	360
aatTTtactt	gaattaaaac	ctttactgat	ttttaactaa	aacggagacc	aaaagaaatc	420
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tattttaaac	tttagtatat	aaaacattat	aattcataat	ataaatcgat	tattttacac	600
gatctcagcc	taaaagcggg	aatatgcacg	ctctgagcat	ggcccaagct	ccacgttaac	660
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caaagc						1626

<210> 21
 <211> 27
 <212> DNA
 <213> Zea mays

<400> 21						
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<210> 22
 <211> 27

<212> DNA
<213> Zea mays

<400> 22
tctcgcattt gcagaaacga acaacgt

27

<210> 23
<211> 525
<212> DNA
<213> Zea mays

<220>
<221> promoter
<222> (1) ... (525)
<223> mLIP15

<400> 23
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tcgcccctct ccacctgctg atccttcgcc atctctccat ctctctttct ctctgagata 420
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caccaaacac aagtcccctt gttcaatccg acaagacaag catcc 525

<210> 24
<211> 587
<212> DNA
<213> Zea mays

<220>
<221> promoter
<222> (1) ... (587)
<223> ESR promoter

<400> 24
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tcatttatgg tacgggatta ataggttcca agaaccagcc acaatccatt tattagtttc 180
atataaatgt cataaatttt tactaaaatt ttctctgtat agtaacatgt cataactgaa 240
cttgtgagaa aaacgccagt tatttatggg acgggattaa taggttccaa aaaccagccg 300
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catttgaaatt tggatttgca ttgtcagtcg ggccagtcga ggggacc 587

<210> 25
<211> 900
<212> DNA
<213> Zea mays

<220>
<221> promoter
<222> (1) ... (900)
<223> PCNA2 promoter

<400> 25

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<210> 26

<211> 1560

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (1)... (1560)

<400> 26

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1 5 10 15

gcg ctc gcc agg ctg acc atg cac gtc ccc gac gag gac atg cta tcg 96
Ala Leu Ala Arg Leu Thr Met His Val Pro Asp Glu Asp Met Leu Ser
20 25 30

ccc ctc gcc gcg ctg cgc ctc gac ggt cat ttc agc ttc cat gac gtc 144
Pro Leu Gly Ala Leu Arg Leu Asp Gly His Phe Ser Phe His Asp Val
35 40 45

tcc gcc atg gcg cgg gac ttc ggc aac cag tgc agc ttc ctg ccg gcc 192
Ser Ala Met Ala Arg Asp Phe Gly Asn Gln Cys Ser Phe Leu Pro Ala
50 55 60

gcc gtg ctc cac cca ggc tcg gtc tcc gat atc gcc gcc acc gtg agg 240
Ala Val Leu His Pro Gly Ser Val Ser Asp Ile Ala Ala Thr Val Arg
65 70 75 80

cac gtc ttc tcc ctg ggc gag ggc tcg ccg ctc acc gtc gcg gcg cgc 288
His Val Phe Ser Leu Gly Glu Gly Ser Pro Leu Thr Val Ala Ala Arg
85 90 95

ggg cat gga cac tcc ctc atg ggt cag tcc cag gcc gcc cag ggg atc 336
Gly His Gly His Ser Leu Met Gly Gln Ser Gln Ala Ala Gln Gly Ile
100 105 110

gtg gtc agg atg gag tcg ctc cgg ggc gct agg ctc cag gtc cac gac 384
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Val	Val	Arg	Met	Glu	Ser	Leu	Arg	Gly	Ala	Arg	Leu	Gln	Val	His	Asp		
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Gly	Phe	Val	Asp	Ala	Pro	Gly	Gly	Glu	Leu	Trp	Ile	Asn	Val	Leu	Arg		
	130					135					140						
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Glu	Thr	Leu	Lys	His	Gly	Leu	Ala	Pro	Lys	Ser	Trp	Thr	Asp	Tyr	Leu		
145					150					155					160		
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His	Leu	Thr	Val	Gly	Gly	Thr	Leu	Ser	Asn	Ala	Gly	Val	Ser	Gly	Gln		
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			180					185					190				
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Val	Thr	Gly	Arg	Gly	Asp	Val	Val	Thr	Cys	Ser	Pro	Glu	Asp	Asn	Ser		
	195					200						205					
gat	ctc	ttc	tat	gct	gct	ctc	ggc	ggc	ctt	ggc	cag	ttc	ggg	atc	ata	672	
Asp	Leu	Phe	Tyr	Ala	Ala	Leu	Gly	Gly	Leu	Gly	Gln	Phe	Gly	Ile	Ile		
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Thr	Arg	Ala	Arg	Ile	Ala	Leu	Glu	Pro	Ala	Pro	Glu	Met	Val	Arg	Trp		
225					230					235					240		
ata	aga	gtt	ctt	tac	tcg	gat	ttt	gaa	agc	ttc	acc	gaa	gac	cag	gag	768	
Ile	Arg	Val	Leu	Tyr	Ser	Asp	Phe	Glu	Ser	Phe	Thr	Glu	Asp	Gln	Glu		
				245					250					255			
atg	ttg	atc	atg	gca	gag	aac	tcc	ttt	gac	tac	att	gaa	ggc	ttt	gtc	816	
Met	Leu	Ile	Met	Ala	Glu	Asn	Ser	Phe	Asp	Tyr	Ile	Glu	Gly	Phe	Val		
			260					265					270				
atc	ata	aac	agg	aca	ggc	atc	ctc	aac	aac	tgg	agg	gcg	tcc	ttc	aag	864	
Ile	Ile	Asn	Arg	Thr	Gly	Ile	Leu	Asn	Asn	Trp	Arg	Ala	Ser	Phe	Lys		
		275				280						285					
cca	cag	gac	cca	gtc	caa	gca	agc	cat	ttc	cag	tca	gat	gga	aga	gtg	912	
Pro	Gln	Asp	Pro	Val	Gln	Ala	Ser	His	Phe	Gln	Ser	Asp	Gly	Arg	Val		
	290					295					300						
cta	tac	tgc	ctc	gaa	cta	acc	aag	aac	ttc	aat	agt	ggc	gac	act	gat	960	
Leu	Tyr	Cys	Leu	Glu	Leu	Thr	Lys	Asn	Phe	Asn	Ser	Gly	Asp	Thr	Asp		
305					310					315					320		
acc	atg	gaa	cag	gaa	gtt	gct	gta	ctg	cta	tct	cgg	ctt	aga	ttc	ata	1008	
Thr	Met	Glu	Gln	Glu	Val	Ala	Val	Leu	Leu	Ser	Arg	Leu	Arg	Phe	Ile		
				325				330						335			
cag	tct	act	cta	ttc	cac	acc	gat	gtc	acg	tac	ctg	gag	ttt	ttg	gac	1056	
Gln	Ser	Thr	Leu	Phe	His	Thr	Asp	Val	Thr	Tyr	Leu	Glu	Phe	Leu	Asp		
			340					345					350				

agg gtg cac acc tct gag ctg aag ctg agg gca caa agc ctc tgg gaa	1104
Arg Val His Thr Ser Glu Leu Lys Leu Arg Ala Gln Ser Leu Trp Glu	
355 360 365	
ggt cca cac cct tgg ttg aat ctt ctg ata ccg agg agc tca atc cgc	1152
Val Pro His Pro Trp Leu Asn Leu Leu Ile Pro Arg Ser Ser Ile Arg	
370 375 380	
aga ttt gct acg gaa gtc ttt ggc agg atc ctg aaa gat agc aac aat	1200
Arg Phe Ala Thr Glu Val Phe Gly Arg Ile Leu Lys Asp Ser Asn Asn	
385 390 395 400	
ggt cct ata ttg ctt tat cca gtg aac aaa tca aag tgg gac aac aaa	1248
Gly Pro Ile Leu Leu Tyr Pro Val Asn Lys Ser Lys Trp Asp Asn Lys	
405 410 415	
acg tca gtg gtc ata cca gat gag gaa att ttc tac cta gtg gga ttc	1296
Thr Ser Val Val Ile Pro Asp Glu Glu Ile Phe Tyr Leu Val Gly Phe	
420 425 430	
ctt tct tca gca ccg tct ctc tca ggt cac ggc agc att gca cat gcg	1344
Leu Ser Ser Ala Pro Ser Leu Ser Gly His Gly Ser Ile Ala His Ala	
435 440 445	
atg agc ctg aac agc caa ata gta gag ttc tgt gaa gag gct gat att	1392
Met Ser Leu Asn Ser Gln Ile Val Glu Phe Cys Glu Glu Ala Asp Ile	
450 455 460	
ggg atg aaa cag tat cta gca cac tac acc aca cag gag cag tgg aaa	1440
Gly Met Lys Gln Tyr Leu Ala His Tyr Thr Thr Gln Glu Gln Trp Lys	
465 470 475 480	
acc cac ttt gga gca agg tgg gag aca ttt gaa cgg agg aaa cac aga	1488
Thr His Phe Gly Ala Arg Trp Glu Thr Phe Glu Arg Arg Lys His Arg	
485 490 495	
tat gat ccc cta gcc atc cta gca cca gga cag aga ata ttc cca aag	1536
Tyr Asp Pro Leu Ala Ile Leu Ala Pro Gly Gln Arg Ile Phe Pro Lys	
500 505 510	
gcg tca ctc cca ttg tct ttg tga	1560
Ala Ser Leu Pro Leu Ser Leu *	
515	

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 <212> PRT
 <213> Zea mays

<400> 27
 Met Lys Pro Pro Ser Leu Val His Cys Phe Lys Leu Leu Val Leu Leu
 1 5 10 15
 Ala Leu Ala Arg Leu Thr Met His Val Pro Asp Glu Asp Met Leu Ser
 20 25 30
 Pro Leu Gly Ala Leu Arg Leu Asp Gly His Phe Ser Phe His Asp Val
 35 40 45

Ser	Ala	Met	Ala	Arg	Asp	Phe	Gly	Asn	Gln	Cys	Ser	Phe	Leu	Pro	Ala	50	55	60
Ala	Val	Leu	His	Pro	Gly	Ser	Val	Ser	Asp	Ile	Ala	Ala	Thr	Val	Arg	65	70	75
His	Val	Phe	Ser	Leu	Gly	Glu	Gly	Ser	Pro	Leu	Thr	Val	Ala	Ala	Arg	85	90	95
Gly	His	Gly	His	Ser	Leu	Met	Gly	Gln	Ser	Gln	Ala	Ala	Gln	Gly	Ile	100	105	110
Val	Val	Arg	Met	Glu	Ser	Leu	Arg	Gly	Ala	Arg	Leu	Gln	Val	His	Asp	115	120	125
Gly	Phe	Val	Asp	Ala	Pro	Gly	Gly	Glu	Leu	Trp	Ile	Asn	Val	Leu	Arg	130	135	140
Glu	Thr	Leu	Lys	His	Gly	Leu	Ala	Pro	Lys	Ser	Trp	Thr	Asp	Tyr	Leu	145	150	155
His	Leu	Thr	Val	Gly	Gly	Thr	Leu	Ser	Asn	Ala	Gly	Val	Ser	Gly	Gln	165	170	175
Ala	Phe	Arg	His	Gly	Pro	Gln	Val	Ser	Asn	Val	Asn	Gln	Leu	Glu	Ile	180	185	190
Val	Thr	Gly	Arg	Gly	Asp	Val	Val	Thr	Cys	Ser	Pro	Glu	Asp	Asn	Ser	195	200	205
Asp	Leu	Phe	Tyr	Ala	Ala	Leu	Gly	Gly	Leu	Gly	Gln	Phe	Gly	Ile	Ile	210	215	220
Thr	Arg	Ala	Arg	Ile	Ala	Leu	Glu	Pro	Ala	Pro	Glu	Met	Val	Arg	Trp	225	230	235
Ile	Arg	Val	Leu	Tyr	Ser	Asp	Phe	Glu	Ser	Phe	Thr	Glu	Asp	Gln	Glu	245	250	255
Met	Leu	Ile	Met	Ala	Glu	Asn	Ser	Phe	Asp	Tyr	Ile	Glu	Gly	Phe	Val	260	265	270
Ile	Ile	Asn	Arg	Thr	Gly	Ile	Leu	Asn	Asn	Trp	Arg	Ala	Ser	Phe	Lys	275	280	285
Pro	Gln	Asp	Pro	Val	Gln	Ala	Ser	His	Phe	Gln	Ser	Asp	Gly	Arg	Val	290	295	300
Leu	Tyr	Cys	Leu	Glu	Leu	Thr	Lys	Asn	Phe	Asn	Ser	Gly	Asp	Thr	Asp	305	310	315
Thr	Met	Glu	Gln	Glu	Val	Ala	Val	Leu	Leu	Ser	Arg	Leu	Arg	Phe	Ile	325	330	335
Gln	Ser	Thr	Leu	Phe	His	Thr	Asp	Val	Thr	Tyr	Leu	Glu	Phe	Leu	Asp	340	345	350
Arg	Val	His	Thr	Ser	Glu	Leu	Lys	Leu	Arg	Ala	Gln	Ser	Leu	Trp	Glu	355	360	365
Val	Pro	His	Pro	Trp	Leu	Asn	Leu	Leu	Ile	Pro	Arg	Ser	Ser	Ile	Arg	370	375	380
Arg	Phe	Ala	Thr	Glu	Val	Phe	Gly	Arg	Ile	Leu	Lys	Asp	Ser	Asn	Asn	385	390	395
Gly	Pro	Ile	Leu	Leu	Tyr	Pro	Val	Asn	Lys	Ser	Lys	Trp	Asp	Asn	Lys	405	410	415
Thr	Ser	Val	Val	Ile	Pro	Asp	Glu	Glu	Ile	Phe	Tyr	Leu	Val	Gly	Phe	420	425	430
Leu	Ser	Ser	Ala	Pro	Ser	Leu	Ser	Gly	His	Gly	Ser	Ile	Ala	His	Ala	435	440	445
Met	Ser	Leu	Asn	Ser	Gln	Ile	Val	Glu	Phe	Cys	Glu	Glu	Ala	Asp	Ile	450	455	460
Gly	Met	Lys	Gln	Tyr	Leu	Ala	His	Tyr	Thr	Thr	Gln	Glu	Gln	Trp	Lys	465	470	475
Thr	His	Phe	Gly	Ala	Arg	Trp	Glu	Thr	Phe	Glu	Arg	Arg	Lys	His	Arg	485	490	495
Tyr	Asp	Pro	Leu	Ala	Ile	Leu	Ala	Pro	Gly	Gln	Arg	Ile	Phe	Pro	Lys	500	505	510

Ala Ser Leu Pro Leu Ser Leu
515

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<211> 1617
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (1)...(1617)

<400> 28
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Met Ala Arg Arg Thr Arg Phe Val Ala Ile Ala Ala Leu Leu Thr Ser
1 5 10 15
ttc ctc aac gtc gca gcc ggg cat tcc cgg cca ctg tcc ggt gcc ggc 96
Phe Leu Asn Val Ala Ala Gly His Ser Arg Pro Leu Ser Gly Ala Gly
20 25 30
ctc ccg ggc gat ctt ttc ggg ctg ggc atc gcg tcg agg atc cgc acg 144
Leu Pro Gly Asp Leu Phe Gly Leu Gly Ile Ala Ser Arg Ile Arg Thr
35 40 45
gac agc aac tcg acg gcg aag gcg gcg acg gac ttc ggc cag atg gtg 192
Asp Ser Asn Ser Thr Ala Lys Ala Ala Thr Asp Phe Gly Gln Met Val
50 55 60
agg gcc gcg ccg gag gcc gtg ttc cac ccc gcc acg ccg gcc gac atc 240
Arg Ala Ala Pro Glu Ala Val Phe His Pro Ala Thr Pro Ala Asp Ile
65 70 75 80
gcc gcg ctc gtc cgg ttc tcc gcc acg tcg gcg gcg ccg ttc ccc gtt 288
Ala Ala Leu Val Arg Phe Ser Ala Thr Ser Ala Ala Pro Phe Pro Val
85 90 95
gcg ccg cgc ggg cag gcc cac tcc tgg cgc gcc cag gcg ctc gcc ccg 336
Ala Pro Arg Gly Gln Gly His Ser Trp Arg Gly Gln Ala Leu Ala Pro
100 105 110
ggc gcc gtc gtc gtg gac atg gcc tcg ctg ggg cgc gcc ccc cgc atc 384
Gly Gly Val Val Val Asp Met Gly Ser Leu Gly Arg Gly Pro Arg Ile
115 120 125
aac gtg tcc gcc gtg gcc gcc gcg gag ccg ttc gtc gac gcc gcc ggc 432
Asn Val Ser Ala Val Ala Gly Ala Glu Pro Phe Val Asp Ala Gly Gly
130 135 140
gag cag ctg tgg gtc gac gtc ctc cgc gcc acg ctg cga cac gcc ctg 480
Glu Gln Leu Trp Val Asp Val Leu Arg Ala Thr Leu Arg His Gly Leu
145 150 155 160
gcg ccc cgc gtg tgg acc gac tac ctc cgg ctc acc gtc gcc gcc acg 528
Ala Pro Arg Val Trp Thr Asp Tyr Leu Arg Leu Thr Val Gly Gly Thr
165 170 175

ctc tcc aac gcg gga atc ggc ggg cag gcg ttc cga cac ggt ccg cag	576
Leu Ser Asn Ala Gly Ile Gly Gly Gln Ala Phe Arg His Gly Pro Gln	
180 185 190	
atc gcc aac gtg cat gaa ctc gac gtc gtc aca ggc aca ggt gag atg	624
Ile Ala Asn Val His Glu Leu Asp Val Val Thr Gly Thr Gly Glu Met	
195 200 205	
gtg aca tgc tcc atg gac gtg aac tcg gac ctg ttc atg gcg gct cta	672
Val Thr Cys Ser Met Asp Val Asn Ser Asp Leu Phe Met Ala Ala Leu	
210 215 220	
ggc ggg tta ggc cag ttc ggg gtc ata acc aga gca cgg atc cgg ctt	720
Gly Gly Leu Gly Gln Phe Gly Val Ile Thr Arg Ala Arg Ile Arg Leu	
225 230 235 240	
gag ccg gcg ccc aag agg gtg cgc tgg gtt cga ctt gcc tac acc gac	768
Glu Pro Ala Pro Lys Arg Val Arg Trp Val Arg Leu Ala Tyr Thr Asp	
245 250 255	
gtc gct act ttc acc aag gat cag gag ttt ctc ata tca aac cgg gct	816
Val Ala Thr Phe Thr Lys Asp Gln Glu Phe Leu Ile Ser Asn Arg Ala	
260 265 270	
agc caa gtc ggg ttc gac tac gtc gaa ggc cag gtc cag ctc agc cgg	864
Ser Gln Val Gly Phe Asp Tyr Val Glu Gly Gln Val Gln Leu Ser Arg	
275 280 285	
tcc ttg gtc gaa ggc ccc aaa tca aca ccc ttc ttc tcc ggc gcc gat	912
Ser Leu Val Glu Gly Pro Lys Ser Thr Pro Phe Phe Ser Gly Ala Asp	
290 295 300	
gtt gct agg ctt gct gga ctc gcg tcc agg acc gga cct gct gca atc	960
Val Ala Arg Leu Ala Gly Leu Ala Ser Arg Thr Gly Pro Ala Ala Ile	
305 310 315 320	
tac tac atc gaa ggc gcc atg tac tac acc aag gac acc gcc ata tct	1008
Tyr Tyr Ile Glu Gly Ala Met Tyr Tyr Thr Lys Asp Thr Ala Ile Ser	
325 330 335	
gtg gac aag aaa atg aag gca ctc ctg gat cag ctg agc ttc gag cca	1056
Val Asp Lys Lys Met Lys Ala Leu Leu Asp Gln Leu Ser Phe Glu Pro	
340 345 350	
ggg ttt gcg ttc acc aag gac gtg acg ttc gtg cag ttc ctc gat cgg	1104
Gly Phe Ala Phe Thr Lys Asp Val Thr Phe Val Gln Phe Leu Asp Arg	
355 360 365	
gtg cgc gag gag gag agg gtg ctc cgg tca gcc ggc gcg tgg gag gtg	1152
Val Arg Glu Glu Glu Arg Val Leu Arg Ser Ala Gly Ala Trp Glu Val	
370 375 380	
ccg cac cca tgg ctg aac ctc ttc gtc cca cgg tcg cgc atc ctc gac	1200
Pro His Pro Trp Leu Asn Leu Phe Val Pro Arg Ser Arg Ile Leu Asp	
385 390 395 400	
ttc gac gac gga gtg ttc aag gct ctg ctc aag gac tcc aac cca gct	1248
Phe Asp Asp Gly Val Phe Lys Ala Leu Leu Lys Asp Ser Asn Pro Ala	

405						410						415						
ggg	atc	atc	ctc	atg	tac	ccc	atg	aac	aag	gat	agg	tgg	gac	gac	cgg	1296		
Gly	Ile	Ile	Leu	Met	Tyr	Pro	Met	Asn	Lys	Asp	Arg	Trp	Asp	Asp	Arg			
			420					425					430					
atg	aca	gcg	atg	acc	cca	gcc	acg	gac	gac	gac	gac	atg	ttc	tat	gcc	1344		
Met	Thr	Ala	Met	Thr	Pro	Ala	Thr	Asp	Asp	Asp	Asp	Met	Phe	Tyr	Ala			
		435					440					445						
gtt	agt	ttc	ctt	tgg	tca	gca	ctg	tcc	gca	gac	gac	gtg	ccc	cag	ctc	1392		
Val	Ser	Phe	Leu	Trp	Ser	Ala	Leu	Ser	Ala	Asp	Asp	Val	Pro	Gln	Leu			
	450						455				460							
gag	aga	tgg	aac	aag	gca	gtg	ctg	gac	ttc	tgt	gat	cgg	tca	gga	ata	1440		
Glu	Arg	Trp	Asn	Lys	Ala	Val	Leu	Asp	Phe	Cys	Asp	Arg	Ser	Gly	Ile			
465					470					475				480				
gaa	tgc	aag	cag	tac	ctg	cca	cac	tac	aca	tct	caa	gac	ggg	tgg	cga	1488		
Glu	Cys	Lys	Gln	Tyr	Leu	Pro	His	Tyr	Thr	Ser	Gln	Asp	Gly	Trp	Arg			
			485					490						495				
cgg	cat	ttc	ggg	gcg	aaa	tgg	agc	agg	atc	gct	gag	ctg	aag	gcc	aga	1536		
Arg	His	Phe	Gly	Ala	Lys	Trp	Ser	Arg	Ile	Ala	Glu	Leu	Lys	Ala	Arg			
		500						505					510					
tat	gac	cct	cgg	gca	ttg	ttg	tgc	ccg	ggc	cag	agg	att	ttt	ccg	gtg	1584		
Tyr	Asp	Pro	Arg	Ala	Leu	Leu	Ser	Pro	Gly	Gln	Arg	Ile	Phe	Pro	Val			
		515					520					525						
cca	gta	gag	gca	tct	ggc	att	gct	tct	gcc	tga						1617		
Pro	Val	Glu	Ala	Ser	Gly	Ile	Ala	Ser	Ala	*								
	530				535													

<210> 29
 <211> 538
 <212> PRT
 <213> Zea mays

<400> 29
 Met Ala Arg Arg Thr Arg Phe Val Ala Ile Ala Ala Leu Leu Thr Ser
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 Phe Leu Asn Val Ala Ala Gly His Ser Arg Pro Leu Ser Gly Ala Gly
 20 25 30
 Leu Pro Gly Asp Leu Phe Gly Leu Gly Ile Ala Ser Arg Ile Arg Thr
 35 40 45
 Asp Ser Asn Ser Thr Ala Lys Ala Ala Thr Asp Phe Gly Gln Met Val
 50 55 60
 Arg Ala Ala Pro Glu Ala Val Phe His Pro Ala Thr Pro Ala Asp Ile
 65 70 75 80
 Ala Ala Leu Val Arg Phe Ser Ala Thr Ser Ala Ala Pro Phe Pro Val
 85 90 95
 Ala Pro Arg Gly Gln Gly His Ser Trp Arg Gly Gln Ala Leu Ala Pro
 100 105 110
 Gly Gly Val Val Val Asp Met Gly Ser Leu Gly Arg Gly Pro Arg Ile
 115 120 125
 Asn Val Ser Ala Val Ala Gly Ala Glu Pro Phe Val Asp Ala Gly Gly

130		135		140
Glu Gln Leu Trp Val Asp Val Leu Arg Ala Thr Leu Arg His Gly Leu				
145		150		155
Ala Pro Arg Val Trp Thr Asp Tyr Leu Arg Leu Thr Val Gly Gly Thr				160
	165		170	175
Leu Ser Asn Ala Gly Ile Gly Gly Gln Ala Phe Arg His Gly Pro Gln				
	180		185	190
Ile Ala Asn Val His Glu Leu Asp Val Val Thr Gly Thr Gly Glu Met				
	195	200		205
Val Thr Cys Ser Met Asp Val Asn Ser Asp Leu Phe Met Ala Ala Leu				
	210	215		220
Gly Gly Leu Gly Gln Phe Gly Val Ile Thr Arg Ala Arg Ile Arg Leu				
225		230		235
Glu Pro Ala Pro Lys Arg Val Arg Trp Val Arg Leu Ala Tyr Thr Asp				240
	245		250	255
Val Ala Thr Phe Thr Lys Asp Gln Glu Phe Leu Ile Ser Asn Arg Ala				
	260		265	270
Ser Gln Val Gly Phe Asp Tyr Val Glu Gly Gln Val Gln Leu Ser Arg				
	275	280		285
Ser Leu Val Glu Gly Pro Lys Ser Thr Pro Phe Phe Ser Gly Ala Asp				
	290	295		300
Val Ala Arg Leu Ala Gly Leu Ala Ser Arg Thr Gly Pro Ala Ala Ile				
305		310		315
Tyr Tyr Ile Glu Gly Ala Met Tyr Tyr Thr Lys Asp Thr Ala Ile Ser				
	325		330	335
Val Asp Lys Lys Met Lys Ala Leu Leu Asp Gln Leu Ser Phe Glu Pro				
	340		345	350
Gly Phe Ala Phe Thr Lys Asp Val Thr Phe Val Gln Phe Leu Asp Arg				
	355		360	365
Val Arg Glu Glu Glu Arg Val Leu Arg Ser Ala Gly Ala Trp Glu Val				
	370	375		380
Pro His Pro Trp Leu Asn Leu Phe Val Pro Arg Ser Arg Ile Leu Asp				
385		390		395
Phe Asp Asp Gly Val Phe Lys Ala Leu Leu Lys Asp Ser Asn Pro Ala				
	405		410	415
Gly Ile Ile Leu Met Tyr Pro Met Asn Lys Asp Arg Trp Asp Asp Arg				
	420		425	430
Met Thr Ala Met Thr Pro Ala Thr Asp Asp Asp Asp Met Phe Tyr Ala				
	435		440	445
Val Ser Phe Leu Trp Ser Ala Leu Ser Ala Asp Asp Val Pro Gln Leu				
	450		455	460
Glu Arg Trp Asn Lys Ala Val Leu Asp Phe Cys Asp Arg Ser Gly Ile				
465		470		475
Glu Cys Lys Gln Tyr Leu Pro His Tyr Thr Ser Gln Asp Gly Trp Arg				
	485		490	495
Arg His Phe Gly Ala Lys Trp Ser Arg Ile Ala Glu Leu Lys Ala Arg				
	500		505	510
Tyr Asp Pro Arg Ala Leu Leu Ser Pro Gly Gln Arg Ile Phe Pro Val				
	515		520	525
Pro Val Glu Ala Ser Gly Ile Ala Ser Ala				
	530		535	

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 <211> 1566
 <212> DNA
 <213> Zea mays

<220>

<221> CDS

<222> (1)...(1566)

<400> 30

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1 5 10 15	
gac gcc ggc cgc gag ccc gcc acc atg gcg ggc ggg tgc gcg gcg gcg	96
Asp Ala Gly Arg Glu Pro Ala Thr Met Ala Gly Gly Cys Ala Ala Ala	
20 25 30	
gcg acg gat ttc ggc ggg ctg ggg agc gcc atg ccc gcg gcc gtg gtc	144
Ala Thr Asp Phe Gly Gly Leu Gly Ser Ala Met Pro Ala Ala Val Val	
35 40 45	
cgc ccg gcg agc gcg gac gac gtg gcc agc gcc atc cgc gcg gcg gcg	192
Arg Pro Ala Ser Ala Asp Asp Val Ala Ser Ala Ile Arg Ala Ala Ala	
50 55 60	
ctg acg ccg cac ctc acc gtg gcc gcc cgc ggg aac ggg cac tcg gtg	240
Leu Thr Pro His Leu Thr Val Ala Ala Arg Gly Asn Gly His Ser Val	
65 70 75 80	
gcc ggc cag gcc atg gcc gag ggc ggg ctg gtc ctc gac atg cgc tcg	288
Ala Gly Gln Ala Met Ala Glu Gly Gly Leu Val Leu Asp Met Arg Ser	
85 90 95	
ctc gcg gcg ccg tcc cgg cgc gcg cag atg cag ctc gtc gtg cag tgc	336
Leu Ala Ala Pro Ser Arg Arg Ala Gln Met Gln Leu Val Val Gln Cys	
100 105 110	
ccc gac ggc ggc ggc ggc cgc cgc tgc ttc gcc gac gtc ccc ggc ggc	384
Pro Asp Gly Gly Gly Gly Arg Arg Cys Phe Ala Asp Val Pro Gly Gly	
115 120 125	
gcg ctc tgg gag gag gtg ctc cac tgg gcc gtc gac aac cac ggg ctc	432
Ala Leu Trp Glu Glu Val Leu His Trp Ala Val Asp Asn His Gly Leu	
130 135 140	
gcc ccg gcg tcc tgg acg gac tac ctc cgc ctc acc gtg ggc ggc acg	480
Ala Pro Ala Ser Trp Thr Asp Tyr Leu Arg Leu Thr Val Gly Gly Thr	
145 150 155 160	
ctc tcc aat ggc ggc gtc agc ggc cag tcc ttc cgc tac ggg ccc cag	528
Leu Ser Asn Gly Gly Val Ser Gly Gln Ser Phe Arg Tyr Gly Pro Gln	
165 170 175	
gtg tcc aac gtg gcc gag ctc gag gtg gtc acc ggc gac ggc gag cgc	576
Val Ser Asn Val Ala Glu Leu Glu Val Val Thr Gly Asp Gly Glu Arg	
180 185 190	
cgc gtc tgc tcg ccc tcc tcc cac ccg gac ctc ttc ttc gcc gtg ctc	624
Arg Val Cys Ser Pro Ser Ser His Pro Asp Leu Phe Phe Ala Val Leu	
195 200 205	
ggc ggg ctc ggc cag ttt ggc gtc atc acg cgc gcc cgc atc ccg ctc	672

Gly	Gly	Leu	Gly	Gln	Phe	Gly	Val	Ile	Thr	Arg	Ala	Arg	Ile	Pro	Leu		
210						215					220						
cac	agg	gcg	ccc	aag	gcg	gtg	cgg	tgg	acg	cgc	gtg	gtg	tac	gcg	agc	720	
His	Arg	Ala	Pro	Lys	Ala	Val	Arg	Trp	Thr	Arg	Val	Val	Tyr	Ala	Ser		
225					230					235					240		
atc	gcg	gac	tac	acg	gcg	gac	gcg	gag	tgg	ctg	gtg	acg	cgg	ccc	ccc	768	
Ile	Ala	Asp	Tyr	Thr	Ala	Asp	Ala	Glu	Trp	Leu	Val	Thr	Arg	Pro	Pro		
				245					250					255			
gac	gcg	gcg	ttc	gac	tac	gtg	gag	ggc	ttc	gcg	ttc	gtg	aac	agc	gac	816	
Asp	Ala	Ala	Phe	Asp	Tyr	Val	Glu	Gly	Phe	Ala	Phe	Val	Asn	Ser	Asp		
			260					265					270				
gac	ccc	gtg	aac	ggc	tgg	ccg	tcc	gtg	ccc	atc	ccc	ggc	ggc	gcc	cgc	864	
Asp	Pro	Val	Asn	Gly	Trp	Pro	Ser	Val	Pro	Ile	Pro	Gly	Gly	Ala	Arg		
		275					280					285					
ttc	gac	ccg	tcc	ctc	ctc	ccc	gcc	ggc	gcc	ggc	ccc	gtc	ctc	tac	tgc	912	
Phe	Asp	Pro	Ser	Leu	Leu	Pro	Ala	Gly	Ala	Gly	Pro	Val	Leu	Tyr	Cys		
	290					295					300						
ctg	gag	gtg	gcc	ctg	tac	cag	tac	gcg	cac	cgg	ccc	gac	gac	gac	gac	960	
Leu	Glu	Val	Ala	Leu	Tyr	Gln	Tyr	Ala	His	Arg	Pro	Asp	Asp	Asp	Asp		
305					310				315					320			
gag	gag	gac	cag	gcg	gcg	gtg	acc	gtg	agc	cgg	atg	atg	gcg	ccg	ctc	1008	
Glu	Glu	Asp	Gln	Ala	Ala	Val	Thr	Val	Ser	Arg	Met	Met	Ala	Pro	Leu		
			325						330					335			
aag	cac	gtg	cgg	ggc	ctg	gag	ttc	gcg	gcg	gac	gtc	ggg	tac	gtg	gac	1056	
Lys	His	Val	Arg	Gly	Leu	Glu	Phe	Ala	Ala	Asp	Val	Gly	Tyr	Val	Asp		
		340					345					350					
ttc	ctg	tcc	cgc	gtg	aac	cgg	gtg	gag	gag	gag	gcc	cgg	cgc	aac	ggc	1104	
Phe	Leu	Ser	Arg	Val	Asn	Arg	Val	Glu	Glu	Glu	Ala	Arg	Arg	Asn	Gly		
		355				360						365					
agc	tgg	gac	gcg	ccg	cac	ccg	tgg	ctc	aac	ctc	ttc	gtc	tcc	gcg	cgc	1152	
Ser	Trp	Asp	Ala	Pro	His	Pro	Trp	Leu	Asn	Leu	Phe	Val	Ser	Ala	Arg		
	370					375					380						
gac	atc	gcc	gac	ttc	gac	cgc	gcc	gtc	atc	aag	ggc	atg	ctc	gcc	gac	1200	
Asp	Ile	Ala	Asp	Phe	Asp	Arg	Ala	Val	Ile	Lys	Gly	Met	Leu	Ala	Asp		
385					390					395				400			
ggc	atc	gac	ggg	ccc	atg	ctc	gtc	tac	cct	atg	ctc	aag	agc	aag	tgg	1248	
Gly	Ile	Asp	Gly	Pro	Met	Leu	Val	Tyr	Pro	Met	Leu	Lys	Ser	Lys	Trp		
				405					410				415				
gac	ccc	aac	acg	tcg	gtg	gcg	ctg	ccg	gag	ggc	gag	gtc	ttc	tac	ctg	1296	
Asp	Pro	Asn	Thr	Ser	Val	Ala	Leu	Pro	Glu	Gly	Glu	Val	Phe	Tyr	Leu		
			420					425					430				
gtg	gcg	ctg	ctg	cgg	ttc	tgc	cgg	agc	ggc	ggg	ccg	gcg	gtg	gac	gag	1344	
Val	Ala	Leu	Leu	Arg	Phe	Cys	Arg	Ser	Gly	Gly	Pro	Ala	Val	Asp	Glu		
		435					440					445					

ctg	gtg	gcg	cag	aac	ggc	gcc	atc	ctc	cgc	gcc	tgc	cgc	gcc	aac	ggc	1392
Leu	Val	Ala	Gln	Asn	Gly	Ala	Ile	Leu	Arg	Ala	Cys	Arg	Ala	Asn	Gly	
	450					455					460					
tac	gac	tac	aag	gcc	tac	ttc	ccg	agc	tac	cgc	ggc	gag	gcc	gac	tgg	1440
Tyr	Asp	Tyr	Lys	Ala	Tyr	Phe	Pro	Ser	Tyr	Arg	Gly	Glu	Ala	Asp	Trp	
	465				470					475					480	
gcg	cgc	cac	ttc	ggc	gcc	gcc	agg	tgg	agg	cgc	ttc	gtg	gac	cgc	aag	1488
Ala	Arg	His	Phe	Gly	Ala	Ala	Arg	Trp	Arg	Arg	Phe	Val	Asp	Arg	Lys	
				485					490						495	
gcc	cgg	tac	gac	ccg	ctg	gcg	atc	ctc	gcg	ccg	ggc	cag	aag	atc	ttc	1536
Ala	Arg	Tyr	Asp	Pro	Leu	Ala	Ile	Leu	Ala	Pro	Gly	Gln	Lys	Ile	Phe	
			500					505					510			
cct	cgg	gtc	ccg	gcg	tcc	gtc	gcc	gtg	tag							1566
Pro	Arg	Val	Pro	Ala	Ser	Val	Ala	Val	*							
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 <212> PRT
 <213> Zea mays

<400> 31

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Ala	Thr	Asp	Phe	Gly	Gly	Leu	Gly	Ser	Ala	Met	Pro	Ala	Ala	Val	Val	
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Ala	Gly	Gln	Ala	Met	Ala	Glu	Gly	Gly	Leu	Val	Leu	Asp	Met	Arg	Ser	
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Leu	Ala	Ala	Pro	Ser	Arg	Arg	Ala	Gln	Met	Gln	Leu	Val	Val	Gln	Cys	
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Pro	Asp	Gly	Gly	Gly	Gly	Arg	Arg	Cys	Phe	Ala	Asp	Val	Pro	Gly	Gly	
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Leu	Ser	Asn	Gly	Gly	Val	Ser	Gly	Gln	Ser	Phe	Arg	Tyr	Gly	Pro	Gln	
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Val	Ser	Asn	Val	Ala	Glu	Leu	Glu	Val	Val	Thr	Gly	Asp	Gly	Glu	Arg	
			180					185					190			
Arg	Val	Cys	Ser	Pro	Ser	Ser	His	Pro	Asp	Leu	Phe	Phe	Ala	Val	Leu	
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His	Arg	Ala	Pro	Lys	Ala	Val	Arg	Trp	Thr	Arg	Val	Val	Tyr	Ala	Ser	
225					230					235					240	

Ile	Ala	Asp	Tyr	Thr	Ala	Asp	Ala	Glu	Trp	Leu	Val	Thr	Arg	Pro	Pro	
				245					250					255		
Asp	Ala	Ala	Phe	Asp	Tyr	Val	Glu	Gly	Phe	Ala	Phe	Val	Asn	Ser	Asp	
			260					265					270			
Asp	Pro	Val	Asn	Gly	Trp	Pro	Ser	Val	Pro	Ile	Pro	Gly	Gly	Ala	Arg	
		275					280					285				
Phe	Asp	Pro	Ser	Leu	Leu	Pro	Ala	Gly	Ala	Gly	Pro	Val	Leu	Tyr	Cys	
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Leu	Glu	Val	Ala	Leu	Tyr	Gln	Tyr	Ala	His	Arg	Pro	Asp	Asp	Asp	Asp	
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Glu	Glu	Asp	Gln	Ala	Ala	Val	Thr	Val	Ser	Arg	Met	Met	Ala	Pro	Leu	
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Lys	His	Val	Arg	Gly	Leu	Glu	Phe	Ala	Ala	Asp	Val	Gly	Tyr	Val	Asp	
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Phe	Leu	Ser	Arg	Val	Asn	Arg	Val	Glu	Glu	Glu	Ala	Arg	Arg	Asn	Gly	
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Ser	Trp	Asp	Ala	Pro	His	Pro	Trp	Leu	Asn	Leu	Phe	Val	Ser	Ala	Arg	
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Asp	Ile	Ala	Asp	Phe	Asp	Arg	Ala	Val	Ile	Lys	Gly	Met	Leu	Ala	Asp	
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		420						425					430			
Val	Ala	Leu	Leu	Arg	Phe	Cys	Arg	Ser	Gly	Gly	Pro	Ala	Val	Asp	Glu	
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Tyr	Asp	Tyr	Lys	Ala	Tyr	Phe	Pro	Ser	Tyr	Arg	Gly	Glu	Ala	Asp	Trp	
465					470					475					480	
Ala	Arg	His	Phe	Gly	Ala	Ala	Arg	Trp	Arg	Arg	Phe	Val	Asp	Arg	Lys	
		485						490						495		
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Pro	Arg	Val	Pro	Ala	Ser	Val	Ala	Val								
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<210> 32

<211> 1629

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (1)...(1629)

<400> 32

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gtc	ctc	tcc	ctc	tgc	tct	ccg	tac	aaa	ttc	ata	cag	agc	ccc	atg	gac	96
Val	Leu	Ser	Leu	Cys	Ser	Pro	Tyr	Lys	Phe	Ile	Gln	Ser	Pro	Met	Asp	
			20					25					30			
ctg	ggc	ccc	ctg	aac	ctg	ctc	ccc	acc	acc	agc	acc	gcg	gcc	gcg	tcc	144
Leu	Gly	Pro	Leu	Asn	Leu	Leu	Pro	Thr	Thr	Ser	Thr	Ala	Ala	Ala	Ser	

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Ser	Asp	Phe	Gly	Arg	Ile	Leu	Phe	Arg	Ala	Pro	Ala	Ala	Val	Leu	Arg		
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ccc	cag	tcg	ccg	agg	gac	atc	tcc	atg	ctg	ctc	agc	ttc	ctc	tcc	ggc	240	
Pro	Gln	Ser	Pro	Arg	Asp	Ile	Ser	Met	Leu	Leu	Ser	Phe	Leu	Ser	Gly		
65					70					75					80		
tcg	ccc	tcg	ctg	agc	agg	gtc	acg	gtg	gcg	gcc	agg	ggg	gca	ggc	cac	288	
Ser	Pro	Ser	Leu	Ser	Arg	Val	Thr	Val	Ala	Ala	Arg	Gly	Ala	Gly	His		
85					90					95							
tcc	atc	cac	ggg	cag	gcg	cag	gcc	ccg	gac	ggc	att	gtg	gtg	gag	acg	336	
Ser	Ile	His	Gly	Gln	Ala	Gln	Ala	Pro	Asp	Gly	Ile	Val	Val	Glu	Thr		
100					105					110							
cgc	tcc	ttg	ccc	ggc	gag	atg	gag	ttc	cac	cac	gtc	cgc	ggg	gga	ggc	384	
Arg	Ser	Leu	Pro	Gly	Glu	Met	Glu	Phe	His	His	Val	Arg	Gly	Gly	Gly		
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gaa	ggg	cgt	gcc	tcc	tac	gcc	gac	gtg	ggc	ggc	ggg	ggt	ctg	tgg	atc	432	
Glu	Gly	Arg	Ala	Ser	Tyr	Ala	Asp	Val	Gly	Gly	Gly	Val	Leu	Trp	Ile		
130					135					140							
gag	ctc	ctg	gag	cgg	agc	ctg	aag	ctt	ggg	ctg	gct	ccc	agg	tcc	tgg	480	
Glu	Leu	Leu	Glu	Arg	Ser	Leu	Lys	Leu	Gly	Leu	Ala	Pro	Arg	Ser	Trp		
145					150					155					160		
acc	gac	tac	ctc	tac	ctc	act	gtc	ggc	ggg	acg	ctg	tcc	aat	gcc	ggc	528	
Thr	Asp	Tyr	Leu	Tyr	Leu	Thr	Val	Gly	Gly	Thr	Leu	Ser	Asn	Ala	Gly		
165					170					175							
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Ile	Ser	Gly	Gln	Thr	Phe	Lys	His	Gly	Pro	Gln	Ile	Ser	Asn	Val	Leu		
180					185					190							
cag	ctg	gag	gta	gtc	aca	gga	cga	ggg	gag	att	gtg	gaa	tgc	tca	ccc	624	
Gln	Leu	Glu	Val	Val	Thr	Gly	Arg	Gly	Glu	Ile	Val	Glu	Cys	Ser	Pro		
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Ser	Lys	Glu	Ala	Asp	Leu	Phe	Asn	Ala	Val	Leu	Gly	Gly	Leu	Gly	Gln		
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Phe	Gly	Ile	Ile	Thr	Arg	Ala	Arg	Ile	Leu	Leu	Gln	Glu	Ala	Pro	Glu		
225					230					235					240		
aag	gtg	acg	tgg	gtg	agg	gcc	ttc	tac	gac	gac	ttg	ggc	gcc	ttc	acc	768	
Lys	Val	Thr	Trp	Val	Arg	Ala	Phe	Tyr	Asp	Asp	Leu	Gly	Ala	Phe	Thr		
245					250					255							
agg	gac	cag	gag	ctg	ctg	gtg	tcg	att	ccg	gat	tcg	gtg	gac	tac	gtg	816	
Arg	Asp	Gln	Glu	Leu	Leu	Val	Ser	Ile	Pro	Asp	Ser	Val	Asp	Tyr	Val		
260					265					270							

gaa ggg ttc atg gtc ctg aac gag cgg tcc ctc cac agc tcc tcc atc	864
Glu Gly Phe Met Val Leu Asn Glu Arg Ser Leu His Ser Ser Ser Ile	
275 280 285	
gcc ttc ccc gcg agc gtg gac ttc agc ccg gat ttc ggc acc agg agc	912
Ala Phe Pro Ala Ser Val Asp Phe Ser Pro Asp Phe Gly Thr Arg Ser	
290 295 300	
agc cct agg atc tac tac tgc gtc gag ttc gcg gtc cac cac cac cac	960
Ser Pro Arg Ile Tyr Tyr Cys Val Glu Phe Ala Val His His His His	
305 310 315 320	
ggt tac cag cag cag tct cag gcg gcc gtg gag gcc atc tcg agg cgg	1008
Gly Tyr Gln Gln Gln Ser Gln Ala Ala Val Glu Ala Ile Ser Arg Arg	
325 330 335	
atg agc cac atg gcg tcc cag ctg tac agc gtg gag gtg tcc tac ttg	1056
Met Ser His Met Ala Ser Gln Leu Tyr Ser Val Glu Val Ser Tyr Leu	
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gac ttc ctg aac cgg gtc agg atg gag gag gtg agc ctg cgg agc gcc	1104
Asp Phe Leu Asn Arg Val Arg Met Glu Glu Val Ser Leu Arg Ser Ala	
355 360 365	
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Gly Met Trp Glu Glu Val His His Pro Trp Leu Asn Met Phe Val Pro	
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aag gcc ggg gtc gct ggc ttc agg gat ctg ctc atg gac aac gtc tcg	1200
Lys Ala Gly Val Ala Gly Phe Arg Asp Leu Leu Met Asp Asn Val Ser	
385 390 395 400	
ccg gat agc ttc cag ggc ctc atc ctc atc tac cca ctc ctc aga gac	1248
Pro Asp Ser Phe Gln Gly Leu Ile Leu Ile Tyr Pro Leu Leu Arg Asp	
405 410 415	
aag tgg gac acc aac acg tcg gtc gtg atc ccg gac tcc ggg ccc acc	1296
Lys Trp Asp Thr Asn Thr Ser Val Val Ile Pro Asp Ser Gly Pro Thr	
420 425 430	
gcg gac gac ccg gtg atg tac gtg gtc ggc atc ctc agg tcc gcg aac	1344
Ala Asp Asp Pro Val Met Tyr Val Val Gly Ile Leu Arg Ser Ala Asn	
435 440 445	
cct ggt cca gaa gaa gac ggt gac ggc tgc tcc cac cgc tgc ctg cac	1392
Pro Gly Pro Glu Glu Asp Gly Asp Gly Cys Ser His Arg Cys Leu His	
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gag ctc ctc cgc agc cac cgc cgg atc gcc gac gcc gcg gag gcg cgc	1440
Glu Leu Leu Arg Ser His Arg Arg Ile Ala Asp Ala Ala Glu Ala Arg	
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ctc ggc gcc aag cag tac ctg cct cac cac ccg acc ccg gcc cgc tgg	1488
Leu Gly Ala Lys Gln Tyr Leu Pro His His Pro Thr Pro Ala Arg Trp	
485 490 495	
cag cag cac ctg ggc cgg cgc tgg gag cgc ttc gcg gac cgc aag gcc	1536
Gln Gln His Leu Gly Arg Arg Trp Glu Arg Phe Ala Asp Arg Lys Ala	

500	505	510	
cgg ttc gac ccg ctg cgc atc ctg ggg ccc ggc cag ggc ata ttc cct			1584
Arg Phe Asp Pro Leu Arg Ile Leu Gly Pro Gly Gln Gly Ile Phe Pro			
515	520	525	
cgg acg gcc cag gat gct gcc gcc gct gct gcg tac ggg agc tag			1629
Arg Thr Ala Gln Asp Ala Ala Ala Ala Ala Tyr Gly Ser *			
530	535	540	

<210> 33
 <211> 542
 <212> PRT
 <213> Zea mays

<400> 33

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Leu Gly Pro Leu Asn Leu Leu Pro Thr Thr Ser Thr Ala Ala Ala Ser			
35 40 45			
Ser Asp Phe Gly Arg Ile Leu Phe Arg Ala Pro Ala Ala Val Leu Arg			
50 55 60			
Pro Gln Ser Pro Arg Asp Ile Ser Met Leu Leu Ser Phe Leu Ser Gly			
65 70 75 80			
Ser Pro Ser Leu Ser Arg Val Thr Val Ala Ala Arg Gly Ala Gly His			
85 90 95			
Ser Ile His Gly Gln Ala Gln Ala Pro Asp Gly Ile Val Val Glu Thr			
100 105 110			
Arg Ser Leu Pro Gly Glu Met Glu Phe His His Val Arg Gly Gly Gly			
115 120 125			
Glu Gly Arg Ala Ser Tyr Ala Asp Val Gly Gly Gly Val Leu Trp Ile			
130 135 140			
Glu Leu Leu Glu Arg Ser Leu Lys Leu Gly Leu Ala Pro Arg Ser Trp			
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Thr Asp Tyr Leu Tyr Leu Thr Val Gly Gly Thr Leu Ser Asn Ala Gly			
165 170 175			
Ile Ser Gly Gln Thr Phe Lys His Gly Pro Gln Ile Ser Asn Val Leu			
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Gln Leu Glu Val Val Thr Gly Arg Gly Glu Ile Val Glu Cys Ser Pro			
195 200 205			
Ser Lys Glu Ala Asp Leu Phe Asn Ala Val Leu Gly Gly Leu Gly Gln			
210 215 220			
Phe Gly Ile Ile Thr Arg Ala Arg Ile Leu Leu Gln Glu Ala Pro Glu			
225 230 235 240			
Lys Val Thr Trp Val Arg Ala Phe Tyr Asp Asp Leu Gly Ala Phe Thr			
245 250 255			
Arg Asp Gln Glu Leu Leu Val Ser Ile Pro Asp Ser Val Asp Tyr Val			
260 265 270			
Glu Gly Phe Met Val Leu Asn Glu Arg Ser Leu His Ser Ser Ser Ile			
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290 295 300			
Ser Pro Arg Ile Tyr Tyr Cys Val Glu Phe Ala Val His His His His			
305 310 315 320			

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<211> 2001

<212> DNA

<213> Zea mays

<220>

<221> misc_feature

<222> (0)...(0)

<223> Promoter for ZmCkx3

<221> misc_feature

<222> (0)...(0)

<223> n = A, T, C, or G

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aacagaatgt	tgacgaggaa	aaaaaatatg	aagggtgctt	cacacctgtc	actccatgcc	660
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<210> 36

<211> 2448

<212> DNA

<213> Zea mays

<220>

<221> misc_feature

<222> (0)...(0)

<223> promoter for ZmCkx4

<400> 36

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<210> 37

<211> 2346

<212> DNA

<213> Zea mays

<220>

<221> misc_feature

<222> (0)...(0)

<223> promoter for ZmCkx5

<400> 37

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<210> 38

<211> 51

<212> DNA

<213> Zea mays

<400> 38

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<210> 39

<211> 42

<212> DNA

<213> Zea mays

<400> 39

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